SEQUENCE LISTING

Underlining in each sequence indicates location of the chromophore domain. Potential cysteine attachment sites are indicated in boldface.

Cph1: Locus SLR0473 = S6803PHY1 = SYN_PHY (Yeh *et al*, 277:1505-15-8 (1997)), a 748 aa protein.

SEQ ID NO:1

MATTVQLSDQSLRQLETLAIHTAHLIQPHGLVVVLQEPDLTISQISANCTGILGRSPED LLGRTLGEVFDSFQIDPIQSRLTAGQISSLNPSKLWARVMGDDFVIFDGVFHRNSDGL LVCELEPAYTSDNLPFLGFYHMANAALNRLRQQANLRDFYDVIVEEVRRMTGFDR VMLYRFDENNHGDVIAEDKRDDMEPYLGLHYPESDIPQPARRLFIHNPIRVIPDVYG VAVPLTPAVNPSTNRAVDLTESILRSAYHCHLTYLKNMGVGASLTISLIKDGHLWGL IACHHQTPKVIPFELRKACEFFGRVVESNISAQEDTETFDYRVQLAEHEAVLLDKMT TAADFVEGLTNHPDRLLGLTGSQGAAICFGEKLILVGETPDEKAVQYLLQWLENRE VQDVFFTSSLSQIYPDAVNFKSVASGLLAIPIARHNFLLWFRPEVLQTVNWGGDPNH AYEATQEDGKIELHPRQSFDLWKEIVRIQSLPWQSVEIQSALALKKAIVNLILRQAEE LAQLARNLERSNADLKKFAYIASHDLQEPLNQVSNYVQLLEMRYSEALDEDAKDFI DFAVTGVSLMQTLIDDILTYAKVDTQYAQLTFTDVQEVVDKALANLKQRIEESGAEI EVGSMPAVMADQIQLMQVFQNLIANGIKFAGDKSPKIKIWGDRQEDAWVFAVQDN GIGIDPQFFERIFVIFQRLHTRDEYKGTGMGLAICKKIIEGHQGQIWLESNPGEGSTFY FSIPIGN

cph2 Locus SLL0821 (Manabe K, Nakazawa M. J Plant Res. 110: 109-122 (1977))

GB:D64003

SEQ ID NO: 2

MNPNRSLEDFLRNVINKFHRALTLRETLQVIVEEARIFLGVDRVKIYKFASDGSGEVL
AEAVNRAALPSLLGLHFPVEDIPPQAREELGNQRKMIAVDVAHRRKKSHELSGRISP
TEHSNGHYTTVDSCHIQYLLAMGVLSSLTVPVMQDQQLWGIMAVHHSKPRRFTEQ
EWETMALLSKEVSLAITQSQLSRQVHQQQVQEALVQRLETTVAQYGDRPETWQYA
LETVGQAVEADGAVLYIAPDLTGSVAQHYQWNLRFDWGNWLETSLWQELMRGQP

SAAMEPMAAVOSTWEKPRPFTSVAPLPPTNCVPHGYTLGELEQRSDWIAPPESLSAE NFOSFLIVPLAADOOWVGSLILLRKEKSLVKHWAGKRGIDRRNILPRLSFEAWEETQ KLVPTWNRSERKLAQVASTQLYMAITQQFVTRLITQQTAYDPLTQLPNWIIFNRQLT LALLDALYEGKMVGVLVIAMDRFKRINESFGHKTGDGLLQEVADRLNQKLSPLAA YSPLLSRWHGDGFTILLTQISDNQEMIPLCERLLSTFQEPFFLQGQPIYLTASMGISTA PYDGETAESLLKFAEIALTRAKCQGKNTYQFYRPQDSAPMLDRLTLESDLRQALTN QEFVLYFQPQVALDTGKLLGVEALVRWQHPRLGQVAPDVFIPLAEELGLINHLGQW VLETACATHQHFFRETGRRLRMAVNISARQFQDEKWLNSVLECLKRTGMPPEDLEL EITESLMMEDIKGTVVLLHRLREEGVQVAIDDFGTGYSSLSILKQLPIHRLKIDKSFVN DLLNEGADTAIIQYVIDLANGLNLETVAEGIESEAQLQRLQKMGCHLGQGYFLTRPL PAEAMMTYLYYPQILDFGPTPPLRKVALPETETEAGQGNVGDRPLPNSLNRENPWTE KLHDYVLLKERLQQRNVKEKLVLKIANKIRASLNINDILYSTVTEVRQFLNTDRVVL FKFNSQWSGQVVTESHNDFCRSIINDEIDDPCFKGHYLRLYREGRVRAVSDIEKADL ADCHKELLRHYQVKANLVVPVVFN INLWGLLIAHECKTPRYWQEEDLQLLMELAT QVAIAIHQGELYEQLETANIRLQQISSLDALTQVGNRYLFDSTLEREWQRLQRIREPL ALLLCDVDFFKGFNDNYGHPAGDRCLKKIADAMAKVAKRPTDLVARYGGEEFAIIL SETSLEGAINVTEALQVEVANLAIPHTVSGTGHVTLSIGIAVYTPERHINPNALVKAA DLALYEAKAKGRNQWLAYEGSQLPHVDGEV

Cph3. Locus SLL1473 (RcaE Homolog) a 297 a histidine kinase homolog

SEQ ID NO: 3

MGKFLIPIEFVFLAIAMTCYLWHRQNQERRRIEISIKQQTQRERFINQITQHIRQSLNLE
TVLNTTVAEVKTLLQVDRVLIYRIWQDGTGSAITESVNANYPSILGRTFSDEVFPVEY
HQAYTKGKVRAINDIDQDDIEICLADFVKQFGVKSKLVVPILQHNRASSLDNESEFP
YLWGLLITHQCAFTRPWQPWEVELMKQLANQVAIAIQQSELYEQLQQLNKDLENR
VEKRTQQLAATNQSLRMEISERQKTEAALRHTNHTLQSLIAASPRGIFTLNLADQIQI
WNPTAERIFGWTETEIIAHPELLTSNILLEDYQQFKQKVLSGMVSPSLELKCQKKDGS
WIEIVLSAAPLLDSEENIAGLVAVVADITEQKRQAEQIRLLQSVVVNTNDAVVITEAE
PIDDPGPRILYVNEAFTKITGYTAEEMLGKTPRVLQGPKTSRTELDRVRQAISQWQS
VTVEAEVLNDSYKEKKSPLK

S

cph4 Locus SLL1124 (DivJ homolog; PAS domain) A 1372 aa protein that is more similar to rcaE than to cph1[Wilde et al.. FEBS Lett 406: 89-92 (1997). GB:U67397 (D90905 or SLL1124)

SEQ ID NO: 4

MTFAATPREVTASAIQWACLCLPGELSAAEALNRWHRHGQRSWEPP AEAKAFPPWALVLDNDGQLLGLLPDWQLAAALWTEHFSPAIALAELCLPCSLRLDL EKLPSLGEVMQIFATWGYG\DVIPVADRQHQTWGLLSIGNLIRSVNLCQLWQNLPL QVTASPPLCLGTETTLGELVHHCFERQISSFPVVYSSPLLPAAAPRIPLGNVSLSNYFK GPNYGSLGLDNPIGPDLSPTFPI\CTINQTYCHARELLRRQNDDYVIITNISGAFVGWV GPQQWLATVQPDVLLEALQRE\\EMPRIVQHLEARIVWQQQQQQRNQHLIQKLLSR NPNLIYLYDLVKNEIVYLNIPGSLDEGGSGGAPIPNPMVETDPRQDLLLPPRYFGLEE LAALQAHEKKEFNFEFTDGGQSVHXFVVEISAFEIDGSGQTSKILCLAQDVSHGKRA EAALHTKEQQLQTLVNTIADGIVILDNHDKVIYANPMACQMFGLSKEEFLQSQLGLS NRGQTEIGINVSPEEEGIGEIKAVPIHWQGEDCRLVTVRDVTDRQRVLKKLRDSEQIH RSLLEALPNLVWRLSSAGDVWECNQRTLAYFGRRGRKILGNTWQQFIEPGERENVQ RQWRQGIAAQEFFQLECRLWRSDGQYRWHLLQVLPLEDRFGSINGWLASSTDIDDL KEAEKALRNQAQQEKLLSSISQRIRESLKLETILRTTVTEVRRTIHADRVLIHHIQEDG LGTTIAESVVNGQPSVMQMDLSPESFPPECXQRYLNGYIYASRDQLPDCAINCAVQC FTVAESQSRIVAPIVFDHSLWGLLIVHQCSSSRTWQTAEIQLMQSLGNQLAIAIQQSL LYERLQEELSERQRAEQKLLEVNQLQKGIFDVANYMIISTDRRGIISTFNRTAEEILGY TAAELIGQQTPLIFHDQEEMASEAVQLSQQLQQTIRPNSIDMFAIPAIQWGVYEREWT YITKTGDRLPVYVSITALRDDQGKVDGLVGVITDLRRQKQIERERQNLDFVVKNSTE LIVITDLEQKVTFLNQAGQSLIGLENPETAQTTYLSEHISPEYLNFWQMEIIPQVFRSG AWEGEFSLQHYQTAVEIPVTASVFLLQGVNGQHPANLVAIVHDITHIKNAEKRILAA LEAEKELGELRSRFISTTSHEFRTPLAIISSSTGILKKYWPKLDGQRRGQHLERIEESVH HMVELLDDVLTINRAETKYLPFEPQPLDLVSFCRGITDELQSSTEYHGLLFSYDGLGP GEIVAFDPKLLRQILTNLLGNAIKYSPSGQPVEFHLQRRGDVGIFSVQDHGIGIGPEDI PNLFDSFYRGTNVGSIPGTGLGLPIVKKCAELHGGMIT\\TSQLGQGSRFEVELPLWY

cph3 Locus SLL0041 (locus 1001300) An 891 aa protein, methyl-accepting chemotaxis protein I. Homology to tsr in last 250 amino acid residues. GB:D64006 Bilin Binding domain residues 386-550

SEQ ID NO: 5

MAEAFIAENTAVEDVSPNPNPAIDTDALAALTQSAVELTPPPPINLPKV ELPPMQPLAPLMAIADPDNLSPMSTSIQAPTQSGGLSLRNKAVLIALLIGLIPAGVIGG LNLSSVDRLPVPQTEQQVkDSTTKQIRDQILIGLLVTAVGAAFVAYWMVGENTKAQ TALALKAKHSHRNLDQPLAVAGDELAIADQTIDALSAQVEKLRHQQDLSLKQAELL TELSRANLSDIDEIQGVIQKNLDQARALFGCERLVFYYHPRYQPEAMVVQALDLTTQ GLIDSKDPHPWGQEDMPSQIVAINDTSGASISNPHRQWLEQHQVKASLTVPLHRDN YPLGLLMAHHCQRPHQWEMRERQFLQQLTEELQTTLDRANLIQERNESAQQAQILK ELTLKISAAINSEQVFDIAAQEIRI ALKADRVIVYRFDATWAGTVIVESVAEGYPKAL GATIADPCFADSYVEKYRSGRIQATRDIYNAGLTPCHIGQLKPFEVKANLVAPINYK GNLLGLLIAHQCSGPRDWHQNEIDLÄGQLTVQVGLALERSDLLAQQKIAEVEQRQM REKMQKRALELLMEVDPVSRGDLTIRAHVTEDEIGTIADSYNATIESLRRIVTQVQT AASQFTETTDTNEVAVRQLAQQANRQALDVAEALERLQAMNKSIQAVAENAAQAE SAVQRATQTVDQGEDAMNRTVDGIVAIRETVAATAKQVKRLGESSQKISKVVNLIG SFADQTNLLALNAAIEAAHAGEEGRGFAVVADEVRSLARQSAEATAEIAQLVATIQ AETNEVVNAMEAGTEQVVVGTKLVEETRR\$LNQITAVSAQISGLVEAITSAAIEQSQ TSESVTQTMALVAQIADKNSSEASGVSATFKELLAVAQSLQEAVKQFKVQ

cph6 locus SLR1212 (ETR1 homolog; PAS domain) An 844 aa protein, chromophore domain 461-628

SEQ ID NO: 6

MAITAFTLGDFFQANSYIPHGHCYLWQTPLVWLHVSADFFTAIAYYSI
PLTLLYFLRKRQDIPFPNIIFLFSTFILCCGTSHFFDIITIWYPIYWISGTVKASMAIVSII
TVFELIQIVPNALNLKSPTELATLNLALNQEIKERQTAEIALQELNNNLEKRVEDRTT
QLAKINQQLEQEIEDKTRAKEDLEKNKDQLAQLAAIVESSQDAIISKTLDGNITSWNE
SAERLFGYTAEEMIGSHITKLIPEELILEEDLIAECIRQGQRINTYETQRQRKDGTKIDV
ALTISPIRDEHKNVVGASKIVRDITARLDVENALRESQYFIEKLANYSPQILYILDPIA
WKNIYVNYQSFEILGYTPEEFKNGGTELLLNIVHPDDIPTLYENKNFWQKSQEGQVL

TTEYRMRHKNGSWRWLRSREVVFARDDYGQVTKVLGTAQDISDSKEQEQRLYEQ
GRRESLLREITQRIRQSLDLPTIFNTVVQEIRQFLEADRVVIFQFSPDSDFSVGNIVAES
VLAPFKPIINSAIEETCFSNNYAQRYQQGRIQVIEDIHQSHLRQCHIDFLARLQVRANL
VLPLINDAILWGLLCIHQCDSSRVWEQTEIDLLKQITNQFEIAIQQATLYEQAQQELA
SKNQLFVQLTNELEQKKVLLKEIHHRVKNNLQIMSSLLYLQFSKASPAIQQLSEEYQ
NRIQSMALIHEQLYRSEDLANIDFSQYLKNLTHNICQSYGCNTDSIKIKLLVEQVKVP
LEQSIPLGLIIQELVSNALKHAFFTTEGEISIKFTSMNSHYSLQVWDNGVGISRDIDLE
NTDSLGMQLIYSLTEQLQGELHYEYVGGAQFGLEFSL

cph7 (locus SLR1393, a 950 aa protein chromophore domain 402-620. Contains a histidine kinase tranmitter domain.

SEQ ID NO: 7

MSPSSHGTAVQQAIADQLLEMILQSQDLHNAYRLVVEGLQRGLGVD RVLLVQNAVFPNRQSRLVAQAIAPARDIMLLDEPCADCRWLHLLGQLPHYGLWTV WEGEGEFVQLDPVQGEFCRTLGIKSLLHLPLVINQRHWGVLSLQYLHQARPWPLED QQFAQRIAHLFCLGLMKTELWIHCQNHKNALQTVVAEGQVQRETYLKSAQRERAI ADVIDKIRFALDLRSLFQTTVTEVRKLLVADRVMIIKVRQNKNFSWGEIQAEAQTDD KLCLLPPKERVPLSSRWIDHFAKGLILAMDD TDDQRADFDQSMLALAKANLVVPLF SGDRLWGVLSVHQCDGPRVWESSDIEFALKIÅLNLGVALQQAELLTESQRRSTALQ SALGEVEAQKDYLARIAEEERALTRVIEGIRQTLELQNIFRATSDEVRHLLSCDRVLV YRFNPDWSGEFIHESVAQMWEPLKDLQNNFPLWQDTYLQENEGGRYRNHESLAVG DVETAGFTDCHLDNLRRFEIRAFLTVPVFVGEQLWGLLGAYQNGAPRHWQAREIHL LHQIANQLGVAVYQAQLLARFQEQSKTMENTLADLTAIVDNLADGLLVIDLFGRITR YNPALLAMFDLEGLELLGAGVDAYFPETLNQLLAKPEREEQKLVTADVELSQGRQG QALITSITSHENGCEYPQCLGAVIMIRDVTHEREVER|MKTDFLATVSHELRTPLTSIL GFATVIQDKLNRVIIPELDLAQPHLGKATERVMRNLAIIESEAQRLTVLINDVLDIAK MEAGQESWQEQPCAIGPIIERAIATITPQAQKKNISLQ&DLEPGLPDFIGDENRILQVV LNLLSNAVKFTPKGLITARSHFHQNYLWVEIIDHGPGINPADQEKIFEPFQQGGGDVL TDKPQGTGLGLPICKKIVEHHGGTIGVNSSLGRGSTFYF\$LPVPVPAVETSPAV

Cph8 locus SLR 1969, a 750 aa protein. CHROMOPHORE DOMAIN (156-347). Contains a histidine kinase tranmitter domain. Adenylate cyclase homology SEQ ID NO: 8

MLPAFSPIFRRLLPAV FERLLRFWRTLAQQTGDGVQCFVGDLPSSLK
PPPGPSVLEAEVDHRFALLVSPGQWALLEGEQISPHHYAVSITFAQGIIEDFIQKQNLP
VVAEAMPHRPETPSGPTIAEQLTLGLLEILNSDSTSFSPEPSLQDSLQASQVKLLSQVI
AQIRQSLDLSEILNNAVTAVQKFLFVDRLVIYQFHYSQPSLTPLEENQIPAPRPRQQY
GEVTYEARRSPEIDTMLGIMTENDCFSQVFSYEQKYLKGAVVAVSDIENHYSSSYCL
VGLLQRYQVRAKLVAPIIVEGQLWGLLIAHQCHHPRQWLDSEKNFLGQIGEHLAVA
IVQSLLYSEVQKQKNNFEKRVIERTKELRDTLMAAQAANLLKSQFINNISHELRTPLT
SIIGLSATLLRWFDHPASLPPAKQQYYLLNIQENGKKLLDQINSIIQLSQLESGQTALN
CQSFSLHTLAQTVIHSLLGVAIKQQINLELDYQINVGQDQFCADQERLDQILTQLLNN
ALKFTPAEGTVILRIWKESNQAIFQVEDTGIGINEQQLPVLFEAFKVAGDSYTSFYET
GGVGLALTKQLVELHGGYIEVESSPGQGTIFTTVIPQQNFPPTTKGQVQDKLDAAMP
FNSSVIVIEQDEEIATLICELLTVANYQVIWLIDTTNALQQVELLQPGLIIVDGDFVDV
TEVTRGIKKSRRISKVTVFLLSESLSSAEWQALSQKGIDDYLLKPLQPELLLQRVQSIQ
QEPLR

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